

Result	Query
1	1
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99	99
100	100

1 GAATTCGGGACCCGCCACAGCAGCAGCTGCTGAGCCATGGCTGAAGCGAATGACCA 60

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

Result	Query	
No.	Score	Match Length DB ID Description

1	601.8	94.3	1173	13	BX44567
2	576.8	90.4	1872	12	B1869731
3	569.4	89.2	1057	11	B0067949
4	567	88.2	1044	12	BM809005
5	550.8	87.9	878	12	B1753845
6	559.8	87.7	821	12	B1598390
7	511.4	80.2	534	9	A1590078
8	501.6	78.6	714	12	BC0706432
9	473.7	68.6	472	9	A1077609
10	433.6	66.1	3404	11	AX053330
11	428.4	66.7	843	12	B1692833
12	424.2	66.5	461	10	B9586865
13	420.6	65.9	2066	11	BC027001
14	408.2	64.0	663	9	A1119291
15	404	63.3	855	12	B1331990
16	402.2	63.0	750	13	BC627243
17	401.2	62.9	508	29	CG531840
18	385.4	60.4	526	29	CG565930
19	385.2	60.4	631	10	BB577624
20	385.2	60.4	689	9	A1663400
21	356	55.8	813	10	B1634970
22	354.6	55.6	611	13	B0840137
23	328.6	51.5	386	10	B9588824
24	327.4	51.3	503	10	BP442335
25	313.6	50.7	485	29	CG554707
26	310.6	50.3	522	14	CD0701495
27	316.8	49.7	529	29	CG639018
28	316.6	49.6	543	9	AA261582
29	307.8	48.2	395	14	CB731841
30	302	47.3	701	12	BM995210
31	298.8	46.8	469	10	BM452919
32	292.2	45.8	570	12	BM654389
33	291.4	45.7	570	12	B1598882
34	281	44.0	458	9	AA594274
35	280.6	44.0	420	13	BX468304
36	279	43.7	415	9	A1008939
37	274.2	43.0	458	14	RS4055
38	273.4	42.9	460	9	AA015793
39	267.6	42.9	424	14	H23109
40	263.4	42.9	364	9	AA238828
41	261.8	41.2	642	10	BB829001
42	261.8	41.2	402	10	AA531268
43	251.8	39.5	402	29	CG631313
44	247	38.7	436	10	BB850804
45	246	38.6	309	29	CG496943

					BX44567 BX44567
					B1869731 60313362
					B0067949 AGENCOUR
					BM809005 AGENCOUR
					B1753845 6302752
					B1598390 6032009
					A1590078 cmbc01.x
					BC0706432 6026974
					A1077609 cy26d7.s
					AX053330 M3s machc
					B1692833 60334275
					B9586865 RCL-NN02
					BC027001 M3s machc
					A1119291 w85c07.y
					B1331990 60328439
					B0627243 U1-H-E00
					CG531840 OST15398
					CG565930 OST191133
					B6637624 BB677624
					A1663400 UH32d07.y
					BP5312970 6020734970
					B0040137 AGENCOUR
					BP588824 CM3-NN024
					BP442335 259038 M3s
					CG554707 OST1685949
					CD0701495 EST18019
					CG239018 OST1406978
					AA261582 m87c09.x
					CB778814 AMGNIC.S
					BM995210 U1-H-BD0
					AA529195 BM98609.y
					BM654389 BS0000090
					B1598882 G0317981
					AA594274 n19G01.8
					DX468304 DMK2p86G6

RESULT 1	1173 bp	msna	linear	BST 15-MAY-2001
BX444567	1173 bp	msna	linear	BST 15-MAY-2001
LOCUS	1173 bp	msna	linear	BST 15-MAY-2001
DEFINITION	1173 bp	msna	linear	BST 15-MAY-2001
CDSDN003YPL6 5'-PRIME, mRNA sequence.	1173 bp	msna	linear	BST 15-MAY-2001

SOURCE ORGANISM	<i>Homo sapiens</i> (human)
REFERENCE	Bakurov et al., Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 1175)
AUTHORS	Li W. B., Gruber, C. C., Jesse, J. and Polayes, D.
JOURNAL TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished (2001)
COMMENT	Contact: Genoscope

name="Homo sapiens ADLIT BRAIN"
/cclote/Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five primers
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized.*

Query Match	94.3%	Score 601.8;	DB 13;	Length 1173;
Best Local Similarity	98.6%;	Pred. No. 6.9e-166;		
Matches 628;	Conservative	0;	Mismatches 7;	Indels 2;
			Gaps	2

QY	3	ATTGCGGAAGCGCCGACACACACGACGCTCTGACCCATGCGCTGAAAGGGAATAATGACACG	62
Db	112	AGTCCTTAAAGGCGCCGACACACGACGCTCTGACCCATGCGCTGAAAGGGAATAATGACACG	19
QY	63	TTGACAGCCCTGACGGAAGTTTATCTGCTCAGCGGAATTACAGAAAGCCCAATCT	12
Db	192	TTGACAGCCCTGACGGAAGTTTATCTGCTCAGCGGAATTACAGAAAGCCCAATCT	25
QY	123	CTCTACTGTAGCAAAAGGGGGCCGACTCTGTAGAGATCTTCCGAGTGGCAATGGATGCG	18
Db	252	CTCTACTGTAGCAAAAGGGGGCCGACTCTGTAGAGATCTTCCGAGTGGCAATGGATGCG	31
QY	183	ACAGAGGACAGAGGACACAGCAATTCGAGTGGCAATCTAGTCCGAAAGCTGTGGGGAG	24
Db	312	ACAGAGGACAGAGGACACAGCAATTCGAGTGGCAATCTAGTCCGAAAGCTGTGGGGAG	37
QY	243	GTGTATATTAAGATGACCCAGATGCGAGTACGTGCGGATGAGACACGAGCGCTTTTA	30
Db	372	GTGTATATTAAGATGACCCAGATGCGAGTACGTGCGGATGAGACACGAGCGCTTTTA	43
QY	303	TAGCGCTGACAGACCAATATGAGAAATGTTTGTCTGGAAAGGCTGAGAGAGACAT	36
Db	432	TAGCGCTGACAGACCAATATGAGAAATGTTTGTCTGGAAAGGCTGAGAGAGACAT	49
QY	363	TACACACCTATATATGCAAGAGACATGACAGAAATGTGTGTGTGTGCTGACAGAG	42
Db	492	TACACACCTATATATGCAAGAGACATGAGAGAAATGTGTGTGTGTGCTGACAGAG	55
QY	423	AATGGAGAGTGGAAAGCGGCTTCTTAAATCTGACATGAGCCAGAAAGATCTTGTCTC	48
Db	552	AATGGAGAGTGGAAAGCGGCTTCTGACATGACATGTGCGAAGAAAGATCTTGTCTC	61
QY	483	CCCTGTGACGTCTCTGTGATTTAAAGATGTGTCTAGGTGTGACATCTGAGAG	54
Db	612	CCCTGTGACGTCTCTGTGATTTAAAGATGTGTCTGTGATGTGTGACATCTGAGAG	67
QY	542	TTTGAGAGGGGTCTGACATGCTGTGACCCCAAAATGTTCCCTTACCAATGAGTGGCTGA	60
Db	672	TTTGAGAGGGGTCTGACATGCTGTGTAACCAAAATGTTCCCTTACCAATGAGTGGCTGA	73
QY	602	ACCCCGGACCAAGAGCTGAAATTTGTAGACACTT	63
Db	731	ACCCCGGACCAAGAGCTGAAATTTGTAGACACTT	76

RESULT 2				
B1869731				
LOCUS	B1869731	832 bp	mRNA	linear
				EST 11-OCT-2001

1 GAA TTG GGA CCG GCA CAA GCA GCA GCT GCT AAG CCA TGC CTG AAG GGA ATT CAC CA 60

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	
c 1	434	68.0	534	9	A15930078	A15930078 tms8201.x	
	2	434	68.0	821	12	B15839390	B15839390 603253009.x
	3	434	68.0	1014	12	BM6090005	BM6090005 ACENICOUR
c 2	434	68.0	1057	13	BQ0679045	BQ0679045 ACENICOUR	
	5	311	50.3	832	12	BK4454567	BK4454567 BK4454567
	6	311	50.3	832	12	B1669731	B1669731 603193622
c 3	317	49.7	522	14	CD701495	CD701495 ESTI18019	
	7	296	46.4	714	12	BG706412	BG706412 602669744
	8	292	44.8	461	10	BP556665	BP556665 RCI-NN022
c 4	10	282	44.2	876	12	B1753845	B1753845 60302752
	11	279	43.7	611	13	B0840197	B0840197 ACENICOUR
	12	277	43.4	420	13	B0483104	B0483104
c 5	13	277	43.4	420	13	B0483104	B0483104
	14	205	32.4	750	13	B0621243	B0621243
	15	188	25.1	460	9	AA015793	AA015793
c 6	15	188	25.1	570	12	B1598698	B1598698
	16	147	23.0	354	9	A1864448	A1864448
	17	144	22.6	4	9	A1083319	A1083319 y126c07.x
c 7	18	116	18.2	366	10	BP955824	BP955824 CM3-NN024
	19	113	17.7	701	12	BM995210	BM995210 UT-H-ED0
	20	111	17.4	424	14	B23109	B23109 ym51f12.x1
c 8	21	109	17.1	352	12	BG700150	BG700150 602679566
	22	101	15.8	472	9	A1077609	A1077609 UT264007.8
	23	81	12.7	255	14	R56184	R56184 P9465
c 9	24	77	12.1	669	12	B1550213	B1550213 603159318
	25	75	11.8	364	14	R14113	R14113 y169e06.x1
	26	74	11.6	503	10	BP443355	BP443355 y174f06.x1
c 10	27	72	11.3	468	9	AA594774	AA594774
	28	72	11.3	468	14	R54255	R54255 y974f06.x1
	29	72	11.3	462	10	AA207545	AA207545 UT-H-B11
c 11	30	72	11.3	588	12	B0006006	B0006006 UT-H-B11
	31	71	11.1	364	9	A1153975	A1153975 q733c08.x
	32	71	11.0	498	13	BK501193	BK501193 DKPEAD793H
c 12	33	61	9.6	525	29	CG568464	CG568464 OSL195476
	34	59	9.2	242	29	CG558760	CG558760 OSL176686
	35	59	9.2	109	29	CG496943	CG496943 OSL71778
c 13	36	59	9.2	113	29	CG605210	CG605210 OSL781652
	37	59	9.2	144	13	BY348996	BY348996
	38	59	9.2	144	29	CG620633	CG620633 OSL719932
c 14	39	59	9.2	358	13	BY320462	BY320462
	40	59	9.2	358	13	BY320462	BY320462
	41	59	9.2	359	13	BY320462	BY320462
c 15	42	59	9.2	368	13	BY230618	BY230618
	43	59	9.2	373	13	BY235966	BY235966
	44	59	9.2	403	29	CG615113	CG615113 OSL299916
c 16	45	59	9.2	418	13	BY327122	BY327122

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	534 bp	mRNA	linear	EST 21-APR-1995
A1590078/c	A1590078	Umb8c01.x1 MCI C2AP Brn25 Homo sapiens cDNA clone IMAGE:1261304.3 similar to U131361 HEPARIN-BINDING GROWTH FACTOR PRECURSOR 1 (HBMAN)?, mRNA sequence.				
ACCESSION	U131361					

ACCESSION	A1590078	
VERSION	A1590078.1	GI:4599126
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	

REFERENCE AUTHORS TITLE	JOURNAL COMMENT
1 (bases 1 to 513) NCI/NINDS-CMAP http://www.ncbi.nlm.nih.gov/ncicgap . National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/ATGAP), Tumor Gene Index	Unpublished (1998) Contact: Robert Strausberg, Ph.D.

Email: cg88ds-remail.nih.gov
Tissue Procurement: David N. Loufs, M.D., Myrna R. Rosenfeld M.D.

Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAD clone distribution information can be
found through the I.M.A.G.E. Consortium/UMC at:
www-bio.lhml.gov/hbpd/image/image.html
Insert length: 736
Seq primer: -40bp from Cldco
High quality sequence accpi: 455.
Location/Qualifiers
1..534

ORIGIN

Query Match	68.04;	Score 434;	DB 9;	Length 534;
Best Local Similarity	100.04;	Pred. No. 2.2e-211;		
Matches 434;	Conservative	0;	Mismatches	0;
			Indels	

530 GCCCAGCAGCACTGTCAGCATGTCTGAAGGGGAAATACCACTTCAAGGCC 471

Dy	/3 TCACCGAAGTTATCTGCTCCAGGGATTACAGAAGCCCAACTCCTTACTGTAA	132
Ddb	470 TCACCGAAGTTATCTGCTCCAGGGATTACAGAAGCCCAACTCCTTACTGTAA	411

Db

410 GCACCGGGGCGACTTCCTGAGATCTCCGGATGGCACTGTGATGGGACAAAGGACA 351

D5	253	AGAGTTACCGAGACTGGCCACTTGGCCATGGACACCGGCGGCTTTATATACGCTTAC	312
D6	350	CGAGGACCGACCACTTACGCTGACGCTCAGTGGGAAAGCTTGGGGAGGTGTATATTA	291

230 AGAGTATCCGAGACATGGCAGTACTTGGCCATGCAACACGACGGGGCTTTTATAGGGCTCAC 231

232

233 AGACACCAATGAGCAATTTTGTTCCTGGAAAAGGCTGGAGAGAACCATTAACAACCT 372

373 ATATATCCAGAGCATCCAGAGGAATTGCTTTGTGGCCTCAAGAGATTGGAGCT 432
170 ATATATCCAGAGCATCCAGAGGAATTGCTTTGTGGCCTCAAGAGATTGGAGCT

Qy	433	GCAAAAGCGGTCT	446
Db	110	GCAAAAGCGGTCT	97

RESULT 2	
B1598390	
LOCUS	
B1598390	821 bp
	mpna
	linear
	ect at con

Accession	Version	Accession	Version
B1598390	B1598390.1	B1598390	B1598390.1
GI:15491329	GI:15491329	GI:15491329	GI:15491329

SOURCE ORGANISM	Homo sapiens (human)
ORGANISM	Homo sapiens

[illegible]